Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1	("6734023").PN.	USPAT; EPO	OR	OFF	2005/12/16 09:23
L2	1	("6770486").PN.	USPAT; EPO	OR	OFF	2005/12/16 10:17
L3	19	stability same denaturant same (receptor or ligand or antibody)	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/12/16 10:19
L4	5	l3 and (MS or (mass adj1 spectrum$))	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/12/16 10:19
L5	75	stability same urea same (receptor or ligand or antibody)	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/12/16 10:19
L6	18	l5 and (MS or (mass adj1 spectrum$))	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/12/16 10:21
L7	5	l4 and (MS or (mass adj1 spectrum$))	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/12/16 10:23
L8	7529	(436/173,86,89,501,518,811).CCLS.	USPAT; EPO	OR	OFF	2005/12/16 10:24
L9	3	l8 and l3	USPAT; EPO	OR	OFF	2005/12/16 10:25
L10	1	l8 and l4	USPAT; EPO	OR	OFF	2005/12/16 10:25
L11	4	l8 and l5	USPAT; EPO	OR	OFF	2005/12/16 10:25
L12	9	(fold$ same denaturant) same ligand	USPAT; EPO	OR	OFF	2005/12/16 10:25
L13	2	l12 and MS	USPAT; EPO	OR	OFF	2005/12/16 10:26
L14	2	l12 and (MS or (mass adj1 spectrum))	USPAT; EPO	OR	OFF	2005/12/16 10:26

=> hydrogen exhange and interaction and mass
L1 0 FILE AGRICOLA
L2 0 FILE BIOTECHNO
L3 0 FILE CONFSCI
L4 0 FILE HEALSAFE
L5 0 FILE IMSDRUGCONF
L6 0 FILE LIFESCI
L7 0 FILE PASCAL

TOTAL FOR ALL FILES
L8 0 HYDROGEN EXHANGE AND INTERACTION AND MASS

=> deuterium and urea and ligand
L9 0 FILE AGRICOLA
L10 1 FILE BIOTECHNO
L11 0 FILE CONFSCI
L12 0 FILE HEALSAFE
L13 0 FILE IMSDRUGCONF
L14 0 FILE LIFESCI
L15 1 FILE PASCAL

TOTAL FOR ALL FILES
L16 2 DEUTERIUM AND UREA AND LIGAND

=> dup rem
ENTER L# LIST OR (END):l16
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L16
L17 2 DUP REM L16 (0 DUPLICATES REMOVED)

=> d l17 ibib abs total

L17 ANSWER 1 OF 2 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on
STN
ACCESSION NUMBER: 2000-0507759 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2000 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Origin of soft spin structure in Mn formate di-urea
AUTHOR: KUBO Hidenori; ZENMYO Kazuko; TOKITA Masahiko; MATSUMURA Manabu; TAKEDA Kazuyoshi; OOHASHI Toorü; YAMAGATA Kazuo
CORPORATE SOURCE: Fukuoka Institute of Technology, Wajiro, Fukuoka 811-0295 Fukuoka 813-8581, Japan; Department of

Applied Physics, Faculty of Engineering, Kyushu University, Hakozaki, Fukuoka 813-8581, Japan; College of Science and Engineering, Iwaki Meisei University, Iwaki, Fukushima 970-8044, Japan

SOURCE: Journal of the Physical Society of Japan, (2000), 69(8), 2669-2674, 8 refs.
ISSN: 0031-9015 CODEN: JUPSAU

DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Japan
LANGUAGE: English
AVAILABILITY: INIST-149, 354000092639230470
AN 2000-0507759 PASCAL

AB Proton NMR measurements at low temperature show that Mn moment direction in Mn formate di-urea easily changes by temperature as well as the replacement of hydrogen with deuterium atom in urea . The change in the moment direction is due to the competition of the magnetic anisotropy caused by the dipole interaction with the anisotropy caused by the surrounding ligand ions. The observed spin structure of four-fold screw rotations of antiferromagnetic layers is well understood by very small interlayer exchange interactions and magnetic anisotropies. The possibility is pointed out that the dipole interaction between the first nearest neighboring layers is the important origin of the transition to the three-dimensional long range order of this compound.

L17 ANSWER 2 OF 2 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2000:30060770 BIOTECHNO
TITLE: Thermodynamic modulation of light chain amyloid fibril formation
AUTHOR: Kim Y.-S.; Wall J.S.; Meyer J.; Murphy C.; Randolph T.W.; Manning M.C.; Solomon A.; Carpenter J.F.
CORPORATE SOURCE: J.F. Carpenter, School of Pharmacy, Box C238, Univ. of Colorado Hlth. Sci. Center, 4200 E. Ninth Ave., Denver, CO 80262, United States.
E-mail: john.carpenter@uchsc.edu

SOURCE: Journal of Biological Chemistry, (21 JAN 2000), 275/3 (1570-1574), 39 reference(s)
CODEN: JBCHA3 ISSN: 0021-9258

DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 2000:30060770 BIOTECHNO

AB To obtain further insight into the pathogenesis of amyloidosis and develop therapeutic strategies to inhibit fibril formation we investigated: 1) the relationship between intrinsic physical properties (thermodynamic stability and hydrogen-deuterium (H-D) exchange rates) and the propensity of human immunoglobulin light chains to form amyloid fibrils in vitro; and 2) the effects of extrinsically modulating these properties on fibril formation. An amyloid-associated protein readily formed amyloid fibrils in vitro and had a lower free energy of unfolding than a homologous nonpathological protein, which did not form fibrils in vitro. H-D exchange was much faster for the pathological protein, suggesting it had a greater fraction of partially folded molecules. The thermodynamic stabilizer sucrose completely inhibited fibril formation by the pathological protein and shifted the values for its physical parameters to those measured for the nonpathological protein in buffer alone. Conversely, urea sufficiently destabilized the nonpathological protein such that its measured physical properties were equivalent to those of the pathological protein in buffer, and it formed fibrils. Thus, fibril formation by light chains is predominantly controlled by thermodynamic stability; and a rational strategy to inhibit amyloidosis is to design high affinity ligands that specifically increase the stability of the native protein.

=> stability and denaturant
L18 33 FILE AGRICOLA
L19 319 FILE BIOTECHNO
L20 3 FILE CONFSCI
L21 0 FILE HEALSAFE
L22 0 FILE IMSDRUGCONF
L23 209 FILE LIFESCI
L24 107 FILE PASCAL

TOTAL FOR ALL FILES
L25 671 STABILITY AND DENATURANT

=> l25 and mass
L26 3 FILE AGRICOLA
L27 17 FILE BIOTECHNO
L28 0 FILE CONFSCI
L29 0 FILE HEALSAFE
L30 0 FILE IMSDRUGCONF
L31 11 FILE LIFESCI
L32 8 FILE PASCAL

TOTAL FOR ALL FILES
L33 39 L25 AND MASS

=> l33 and ligand
L34 0 FILE AGRICOLA
L35 0 FILE BIOTECHNO
L36 0 FILE CONFSCI
L37 0 FILE HEALSAFE
L38 0 FILE IMSDRUGCONF
L39 0 FILE LIFESCI
L40 0 FILE PASCAL

TOTAL FOR ALL FILES
L41 0 L33 AND LIGAND

=> l33 and interaction
L42 2 FILE AGRICOLA
L43 5 FILE BIOTECHNO
L44 0 FILE CONFSCI
L45 0 FILE HEALSAFE
L46 0 FILE IMSDRUGCONF
L47 4 FILE LIFESCI
L48 2 FILE PASCAL

TOTAL FOR ALL FILES
L49 13 L33 AND INTERACTION

=> dup rem
ENTER L# LIST OR (END):l49
DUPLICATE IS NOT AVAILABLE IN 'IMSDRUGCONF'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L49
L50 8 DUP REM L49 (5 DUPLICATES REMOVED)

=> l50 and urea
L51 2 S L50
L52 1 FILE AGRICOLA
L53 5 S L50
L54 1 FILE BIOTECHNO
L55 0 S L50
L56 0 FILE CONFSCI
L57 0 S L50
L58 0 FILE HEALSAFE
L59 0 S L50
L60 0 FILE IMSDRUGCONF
L61 0 S L50
L62 0 FILE LIFESCI
L63 1 S L50

L64 0 FILE PASCAL

TOTAL FOR ALL FILES
L65 2 L50 AND UREA

=> d l65 ibib abs total

L65 ANSWER 1 OF 2 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN
ACCESSION NUMBER: 2003:46219 AGRICOLA
DOCUMENT NUMBER: IND23332972
TITLE: Evidence that thermodynamic stability of papaya glutamine cyclase is only marginal.
AUTHOR(S): Azarkan, M.; Amrani, A.; Zerhouni, S.; Oberg, K.A.; Ruysschaert, J.M.; Wintjens, R.; Looze, Y.
AVAILABILITY: DNAL (381 B524)
SOURCE: Biopolymers, Dec 5, 2002. Vol. 65, No. 5. p. 325-335
Publisher: New York, N.Y. : John Wiley & Sons, Inc.
CODEN: BIPMAA; ISSN: 0006-3525
NOTE: Includes references
PUB. COUNTRY: New York (State); United States
DOCUMENT TYPE: Article
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English
AB Papaya glutamine cyclase (PQC), a glycoprotein with a molecular mass of 32,980 Da, is a minor constituent of the papaya latex protein fraction. In neutral aqueous solutions, PQC adopts an all-beta conformation and exhibits high resistance to both proteolysis and denaturation. Complete unfolding of PQC requires a combination of an acidic medium and chemical denaturant such as urea or guanidine hydrochloride. The unfolding process takes place through formation of an intermediate A state that accumulates in the absence of chemical denaturants and displays all the features of a molten globule state. The different conformational states--N (native), A (acid-inactivated), and U (unfolded)--have been characterized by means of circular dichroism measurements, fluorescence spectroscopies, Stokes radii determinations, and 8-anilino-1-naphtalenesulfonic acid (ANS) binding characteristics. The unfolding pathways of the enzyme was further studied to estimate thermodynamic parameters characterizing both transitions N reversible reaction A and A reversible reaction U. In its A state, PQC is catalytically inefficient and highly susceptible to proteolysis. Also, its thermodynamic stability is decreased by some 3-5 kcal/mol. Conversion of the native to the A state involves digging up of five amino functions together with protonation of four to five acidic groups with

pKas, in the native state, around 2.7. It proceeds both cooperatively and reversibly although, in vitro, the refolding process is slow. Unfolding of the A state, on the other hand, occurs with a low degree of cooperativity. The intermediate A state thus seems to be only marginally more stable than the unfolded state. The role of suspected internal ion pairs in the stabilization of the native state of this enzyme is discussed.

L65 ANSWER 2 OF 2 BIOTECHNO COPYRIGHT 2005 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1993:23225653 BIOTECHNO
TITLE: Effect of pH and denaturants on the folding and stability of murine interleukin-6
AUTHOR: Ward L.D.; Jian Guo Zhang; Checkley G.; Preston B.; Simpson R.J.
CORPORATE SOURCE: Ludwig Institute for Cancer Research, P.O. Royal Melbourne Hospital,Parkville, Vic. 3050, Australia.
SOURCE: Protein Science, (1993), 2/8 (1291-1300)
CODEN: PRCIEI ISSN: 0961-8368
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AN 1993:23225653 BIOTECHNO
AB The conformation and stability of a recombinant mouse interleukin-6 (mIL- 6) has been investigated by analytical ultracentrifugation, fluorescence spectroscopy, urea-gradient gel electrophoresis, and near- and far- ultraviolet circular dichroism. On decreasing the pH from 8.0 to 4.0, the tryptophan fluorescence of mIL-6 was quenched 40%, the midpoint of the transition occurring at pH 6.9. The change in fluorescence quantum yield was not due to unfolding of the molecule because the conformation of mIL-6, as judged by both urea-gradient gel electrophoresis and CD spectroscopy, was stable over the pH range 2.0-10.0. Sedimentation equilibrium experiments indicated that mIL-6 was monomeric, with a molecular mass of 22,500 Da over the pH range used in these physicochemical studies. Quenching of tryptophan fluorescence (20%) also occurred in the presence of 6 M guanidine hydrochloride upon going from pH 7.4 to 4.0 suggesting that an amino acid residue vicinal in the primary structure to one or both of the two tryptophan residues, Trp-36 and Trp-160, may be partially involved in the quenching of endogenous fluorescence. In this regard, similar results were obtained for a 17-residue synthetic peptide, peptide H1, which corresponds to an N-terminal region of mIL-6 (residues Val-27-Lys-43). The pH-dependent acid quenching of endogenous tryptophan fluorescence of peptide H1 was 30% in the random coil conformation and 60% in the presence of .alpha.-helix-promoting solvents. Replacement of His-33 with Ala-33 in peptide H1 alleviated a significant portion of the

pH-dependent quenching of fluorescence suggesting that the interaction of the imidazole ring of His-33 with the indole ring of Trp-36 is a major determinant responsible for the quenching of the endogenous protein fluorescence of mIL-6.